Program and Abstracts

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Gene copy number variation impacts on gene expression in a multipartite virus

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Abstract

Multipartite viruses have a segmented genome and each segment is encapsidated independently. Earlier studies reported that the distinct genome segments reproducibly accumulate at a specific and host-dependent relative frequency, defined as the 'genome formula'. It has been hypothesized that variations of the genome formula could affect gene expression via changes of the viral gene copy number. The multipartite virus model used in this work is a nanovirus, the faba bean necrotic stunt virus (FBNSV), composed of eight DNA genome segments each encoding a single gene. We initiated twenty parallel FBNSV lineages in faba bean plants, transferred them to medicago plants, and monitored both the relative amounts of the DNA segments and those of the corresponding mRNAs in all lineages. Our analyses showed that the genome formula variations directly impact on gene expression. Moreover, when passaging FBNSV from one host species to the other, we observed that the variation of the genome formula allowed the maintenance of similar proportions of the eight viral mRNAs, suggesting that the genome formula adjusts gene expression to a changing environment. Deep-sequencing analysis of FBNSV lineages similarly alternating from faba bean to medicago host plants demonstrated that the genome formula changes result from the flexibility of this viral system. By this we mean that no DNA sequence mutations could be associated to the genome formula host-dependent switch, which can thus be viewed as a plastic phenomenon. Together, our results indicate that the genome formula adapts gene expression of this multipartite virus in a changing environment in a DNA-sequence mutation-independent way.